

GenCore version 5.1.4-p5-4578  
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### On nucleic - nucleic search, using sw model

Run on: April 15, 2003, 00:17:03 ; Search time 2461.04 Seconds  
(without alignments)  
10930.628 Million cell updates/sec

Title: us-09-001-737-7  
Perfect score: 1661

Sequence: 1 GAAATTCGGCTCATATGCCA.....TGGCGGGATAAGCCGAATTC 1661

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 00000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: em.estba:\*

2: em.estbb:\*

3: em.estin:\*

4: em.estmu:\*

5: em.estov:\*

6: em.estpl:\*

7: em.estro:\*

8: em.htc:\*

9: qb.estl:\*

10: qb.est:\*

11: qb.htc:\*

12: qb.est3:\*

13: qb.estd:\*

14: qb.estj:\*

15: em.esttun:\*

16: em.estom:\*

17: qb.gss:\*

18: em.gss\_hum:\*

19: em.gss\_inv:\*

20: em.gss\_plo:\*

21: em.gss\_vrt:\*

22: em.gss\_fut:\*

23: em.gss\_mam:\*

24: em.gss\_mus:\*

25: em.gss\_other:\*

26: em.gss\_pro:\*

27: em.gss\_rnd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Query	Match Length	DB ID	Description
1	AY109623	11	AY109623	zea mays
2	AY109623	11	AY109623	zea mays
3	AY109623	11	AY109623	zea mays
4	AY109623	11	AY109623	zea mays
5	AY109623	11	AY109623	zea mays
6	AY109623	11	AY109623	zea mays

### ALIGNMENTS

RESULT 1  
AY109623  
LOCUS AY109623 DEFINITION Zea mays CL2221\_1 mRNA sequence. ACCESSION AY109623 VERSION AY109623.1 GI:21213414 KEYWORDS HTC.  
SOURCE  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
Cleide; Panicoidae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 265)  
Hainey,C.R., Dolan,M., Mao,G.H., Vogel,J.M., Whistett,M.S., Arthur,L.W., Haneley,M., Morgan,K. and Tiney,S.V.  
Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes  
Unpublished (2002)  
REFERENCE 2 (bases 1 to 265)  
Coe,E.C.  
TITLE Direct Submission  
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
FEATURES Location/Qualifiers 1..2265  
source /organism="Zea mays"  
/db\_xref="Maizdb630867"  
/clone="CL2221\_1"

	/clone.lib."Maize Mapping Project/Dupont Consensus Library," this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration with the Maize overgo addressing of BACs in conjunction with the Maize Mapping Project"	BASE COUNT	615 a	430 c	559 g	538 t	83 others
Query	Match	Similarity	28.4%	Score	472;	DB	11
Db	913; Matches	56.4%; Pred No. 1	3e-120;	Length	2265;		
Qy	13 ATATGGCAAAAGAACATAAATTCTCACGAGTCGGGTGCGCATGGTGGGACTTG	72		Mismatches	697;	Indels	9;
Db	288 ATGCUGCGAAAGCAGCTCAGTTGGTGGTGGAGCCCGCTGCTGATGNNNNNNNNNNN	347		Gaps.	3;		
Qy	73 ATATGGTAGCACATACCGTCGAAGTAACCTTGCTCTTAAGGGCCTAAGTGTGTTTG	132					
Db	348 NNNNNNNNCAGACATCTGTCGAAGAGACATGGACCTTAAAGGGCCTAAGTGTGTTTG	407					
Qy	133 AAAAGCCTTGGTCTCCCTTAATRACTAATGCAAGGTAAACATGCTAAGAGATGCCG	192					
Db	408 AGCAAGCTTGGTGGCAGCAAGAGATGTTGACTGAGCAAGRCATGGCTTGTGAGCTTGTG	467					
Qy	193 ATATAGAAGATCATUTTGCAAACTGGGCAARTGGTGTGAGGGCTCTTAAAR	252					
Db	468 ATTTAAGGATAGTAAAGATGTTGGTGGCAGCTTGGTGGAGCTTATGCTAA	527					
Qy	253 CCGATGATGATGCTGGTATGGAGACTACGACAGCTTGTGACACGGCTATGTC	312					
Db	528 CTATGACACTCTGGCTGGTGTACCTGTGCTGACTGTGTTGACAAAGCTGATTA	587					
Qy	313 ATGAGGACTAAAAATGTGACAGGGCTPAATCAATTGTTGTTGACAACTGGTCAAGTCA	372					
Db	588 CTGAGGGGTCGAATCTGCTGGTGGATGAAAGCTGATGGTTAAGGGTGTGCGTGTG	647					
Qy	373 AARACGACACGCAACAGCTGTTGACCTTGTGACCTTGTGTCACCTGATCTGCA	432					
Db	648 CAANGCAGTGTGAGCCTTGTGACAACTGCAAAGGATGCCAGAAGTCAACATT	707					
Qy	433 AGGAGGATATGCTCAGTCCTGCTGAGTATCCTACGCTGCTGAA--AAGTGGAGATC	489					
Db	708 CAGARGAAATGCAAGCTGGTGTAAATATGCAACATGGRAAAGGAAATGGAGC	767					
Qy	490 ATATCTCAGAAGCTATGGGGTGTGGCAGCAGGAGTGTGATACATCGAGAAATC	549					
Db	768 TATTGCCAAGGCCTGGAGAGGTGGCAAAAGGGTCACTATGGGAGCTTA	827					
Qy	550 GAGGTAGGAAACAGACTTGTAGCTGGGGTGGGGATCAATTACCTGTGTTACCTG	609					
Db	828 ACACCCCTTATAATGACTGCTGAGTGGGGATGAGTACAGCAGGTAACT	887					
Qy	610 CTGATCATGGTCACAGACAATAAAATGTTGCAAGCTTCAAAACCCATTATCT	669					
Db	888 CTCCGTRACTCTCATACACTCAAAGGCCAGAAATGGAATGGAGCCGATGATC	947					
Qy	670 TAATCAGGATAAAAGTGCACACATCCAGACATTGCACTACTGTGAGGAGTC	729					
Db	948 TAATCTATGACAGAAGGTGAGTACAGTGTGTTAGGTGTTAGAAATGGCCT	1007					
Qy	730 TAAACACCACCCCTCATTACTCTATTGAGGTGCTGATGTTGAGGACTTC	789	RESULT	2			
Db	1008 TGAAGAACACAAAGCCCTACTGATGTTGAGGATGAGATGGAGCTGGCA	1067	AY104969				
Qy	790 CCTTCTCTGACAGCAGATGGTGTACTCTACATGTTGCTCAAGGCCAGT	849	DEFINITION	AY104969			
Db	1068 CTGTGATATGACAGCTCTGCTGAGCTGAGCTGAGTGTGCTGTCAGAGTC	1127	ACCESSION	PC0070542	mRNA	2290 bp	linear
Qy	850 TGGTGTGATGTCCTAAAGCTGTGAGCTGAGCTGAGTGTGCTGTCAGTGA	909	VERSION	AY104969			
			KEYWORDS	A104969.1			
			SOURCE	GI:21208047			
			ORGANISM	Zea mays			
			SEQUENCE	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACC			
			REFERENCE	clade; Panicoidae; Andropogoneae; Zea; 1 (bases 1 to 2290)			
			AUTHORS	Hainey, C. F., Dolan, M., Miao, G. H., Vogel, J. M., Whitsitt, M. S., Arthur, L. W., Hanley, M., Morigante, M. and Tiney, S. V.			
			TITLE	Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes			
			JOURNAL	Published (2002)			
			REFERENCE	2 (bases 1 to 2290)			
			AUTHORS	Cole, E. C.			
			TITLE	Direct Submission			
			JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of			
Db	1128 TGGGGTAAACGGGCAACTACGGACCTGGCATCTACTGGAGGAGTAA	1187					
Qy	910 TTACAGGGCTCTGGGACTGAATTAAGAGTGTACATGACASCCCTTGACAGCTG	959					
Db	1188 TAACTGAGACTCTGGGATGAGTGTGACCTTGAGGTTTGGCTCACATGCTGGTACATGCN	1247					
Qy	970 CTAGAT-TACAGTGTATAAGATGAGCAGCAGTGTGAGTGTGAGTCAGTCAGAG	1029					
Db	1248 NNNGGTTGACTGTRCTPAAGTGAACACTGTTATCTTGATGGAGCCGGAGCAGAGT	107					
Qy	1030 CTATGCTAACCGTATGCACTGTTAATGCAATTAGAACACAACCTCTGACITTG	1089					
Db	1308 CCATGAGAGAGGGCAGACAGATTAGATGACATGACATGAGAATGACACTTCAGAT	1367					
Qy	1090 ACGCTGAAACTACAGAACGTTGGCAAAATAGCTGGGTTAGCTGTTGAGCTGTTGAAAG	1149					
Db	1368 ATAGGAAAGACTCAGGGCTGGCAAGCTCTGCTCTGGAGTTGGTCTGAGTC	1427					
Qy	1150 TAGGACTCTCAAGAGACAGCCTTAAGAAATGAACTTGACCTGATGCTTA	1209					
Db	1428 TGGGGAGCCGGAGCAGAAGTGTGAGGGATGACCTGTTGAGGTTGCTTA	1487					
Qy	1210 ATGCTAACGCTGGCGCTGAGAAGCTGTTGAGCTGTTGAGCTGAGGACTTATPA	1269					
Db	1488 ATGCTACTAAAGCTGTTGAGGGATGTTGACCTGTTGCTCTCTCTCTCT	1547					
Qy	1270 CGTTATTGAAAGTAGCAGCCTGCTGAGTGTG -- AGGGATGATGCTGGGGTA	1326					
Db	1548 ATGCTGAGGAGCTGTTAATTCAGGACCTGAGTGTGAGAATGAGTGTGTC	1607					
Qy	1327 ATATGTTGCTGCTGAGAAGGCTTSTACCTAAATTGCTTAATGTTGAGTAA	1266					
Db	1489 ATGCTACTAAAGCTGTTGAGGGATGTTGACCTGTTGCTGAGTGTGTC	1386					
Qy	1608 AAATCATTCAGATGCTTGTGAGCACCTCTACACACAAATTGCTCAAATGCTG	1667					
Db	1787 AAGGTCCTGACTATGACAG --- TGGAAACAGCCCTGGAGAACAGCTTATG	1443					
Qy	1688 AGGGACGACTAGTGTGAGAATGAGCTGTTGAGCTGTTGTTGAGT	1727					
Qy	1444 CTGCAACAGCTGAGTGTGAGTGTGATGTTAAAGACGATATGACCTGTC	1503					
Db	1728 CTGCTAAAGTGTATGTTGAGCTGAGACGGCTTGTGAGCTGAGTGTGTC	1787					
Qy	1504 CACGATCAGCGCTCAAAATGCACTCTGCTACTGTTGACAGAGAGC	1563					
Db	1788 TCAGACTGCTTGTGGATGCTGAGCTGTTGCTGTCCTGATGACACCCAGGAA	1847					
Qy	1564 TGTGCTATAAACCTGACCGCTACGGCCAGGACATGCGCACAGGTGAT	1622					
Db	1848 TAATGTTGAGATTCCTCAAGGAGGACCGCCCTCAGCATGGTGGCGCAGG	1906					



AUTHORS	Coe, E.C.
TITLE	Direct Submission
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
FEATURES	
SOURCE	
organism	"zea mays"
(ab-xref)	"MaizeDB:633377"
(clone)	"rc063104"
/clone_1.lib	Maize Mapping Project/DuPont Cornsensus Library
Note	"this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize ORIGIN
BASE COUNT	668 a 483 c 643 g 544 t
Query Match	25.9%; Score 430.6; DB 11; Length 2338;
best local similarity	56.2%; Pred. No. 5.2e-109; Matches 875; Conservative 0; Mismatches 669; Indels 13; Gaps 3;
Oy	66 GAGAGTGTAACTGTTAGCAGATACCGTCAGAAGTAGACCTTGCTTAAGGGCGCATGT 125
Db	452 GGAGGCTAACTAACGCTTGAGCAGCTAGTGTGAGTCACTCGACGCCAAGGGAGGAGTC 511
Oy	126 CTTCCTGAANAGCTTGTGCTCCCTTAATCTAACTAATGACGGGTAAACCATGCTCAA 185
Db	512 GTTGGAGAGCACAGTACCGCTCCCAAGATGTTAACGATGCGTACAGTGCAGA 571
Oy	186 GAGATGCAATGAGAGTACATTGAAACATGGCCAATTGCTGCTGAGTGCT 245
Db	572 GAGSTGTGAGCTGGAGCACCTGTTGGAGAACATGGAGCTAACATGGCTGAGTC 631
Oy	246 TCTAAACACGATGATATGCTGTTGTTGAGGAGCAACTGCAACAGTTGACAAAGCC 305
Db	632 GCTTAAAGCACAGCACACGACAGCTGCTGGAGTGGCACACCTCTGGCTG 691
Oy	306 ATGTTCTGAGGACTAAATAATGAGCAGCGAGCTATCATTGTTATCGCGCA 365
Db	692 CTGATTCGCTGGAGGGTTAACTGTGTCAGCTGGCTCATCTTCAGATACCGT 751
Oy	365 GCGATGAAACGACACGACACGACAGCTGTGAGCTTAAACCCATTGCACTGTA 425
Db	752 GTTATCAGAACACGCAAAAGCAACTAGTGTGAGACTACGGAGTTCTGGAGTT 811
Oy	426 TCTGGCAAGGGAGTATGCTCAGTCGCTGAGTATCATCGCCTGAGAAAGTGG 485
Db	812 GAAGATGATGCTGAGCTGAGATGTTCTGCTGTAGTGTGCTGCAACACTATGAATGTT 871
Oy	486 GATGATCTGAGGCTATGAGCTGTTGAGCTGCTGGAGGCTGTTGAGAA 545
Db	872 AACATGATAGCTGAGGCCATGAGCAGGAGCTGGCTGCGAAGGGTTACCCGAGA 931
Oy	546 TCTGGAGTGTGAAACAGACTGTAAGTGTGAGGCTGAGCTGCAATTGACCTGCTAC 605
Db	932 GGAGGAGGCTGAGCTGAGCTTCTTGTTGGAGGAGTGAATTGACCTGGTTAC 991
Oy	, 606 CTGTCATCAATACATGGTCACAGACAGATCAAATAAATGGTGGCGACCTGTTGAGACCTT 665
Db	992 ATCTCAGCGRACTTTGTAACAGAGAGTGAAGATCTGGCGAGGATGACTGCAAG 1051
Oy	666 ATCTTAATCAGGATAAAAGTGTCAACACATCCAGACATTTGCCAC-TACTTGGAA 724
Db	1052 CTCTCTGTTGTTGAGTACACAGATACCAACGAGGATCTATCAAGCTTGGAGA 1111
Oy	725 AGCTCTAAACCAACCGTCATRACTCATTTGAGATGTTGGAGTGGTAAACGCT 784
Db	1112 AGCCATCAGGGCTACATCCCAATCTGATAATGCTGAGGATATGACAGGAGCTC 1171
RESULT	4
LOCUS	BH70613
DEFINITION	1327 bp DNA linear GSS 01-MAY-2002
VERSION	BH70613
ACCESSION	BH70613.1 G:20373570
KEYWORDS	GSS
SOURCE	Lactococcus lactis subsp. cremoris.
ORGANISM	Lactococcus lactis subsp. cremoris.
Bacteria; Firmicutes; Lactobacillales; Streptococaceae;	
REFERENCE	1 (bases 1 to 127)
AUTHORS	Boletin, R., Brilich, S.D. and Sorokin, A.
TITLE	Studies of dairy bacteria Lactococcus lactis

COMMENT	Contact: Sokolkin A Génétique Microbienne INRA CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France Tel: 33 1 34 65 25 16 Fax: 33 1 34 65 25 21 Email: sarkine@jouy.inra.fr best homologue in strain IIL1403 is groEL (93%)
FEATURES	High quality sequence start: 30 Class: shotgun High quality sequence stop: 1399. Location/Qualifiers
SOURCE	/organism="Lactococcus lactis subsp. cremoris" /db_xref="taxon:1359" /clone_id="MG1363" Random Sequence Tag Library" /note="Vector: pSGMU2; Site: 1; Smal; Library of chromosomal fragments of L.lactis strain MG1363 was prepared by partial AluI digestion or by sonication."
BASE COUNT	392 a 292 c 239 g 403 t 1 others
ORIGIN	Query Match 24.9%; Score 414.2; DB 17; Length 1327; Best Local Similarity 72.0%; Pred No. 1 4e-104; 0; Mismatches 214; Indels 1; Gaps 1; Matches 553; Conservative
QY	830 TGTGTCACAGGCCASGATTTGGATGCTGTTAAGACTATCTTGAAAGACATGTCT 889
DB	1322 TCGTGTAAAGCAGCCGGATTGG-CGGCTTAAGGTCAATGGAGATTAGTAT 1264
QY	890 CTGACAGGGTTACAGTATGATACAGGAGATAGGACTGTTAAGATGCTACAT 949
DB	1263 CTGACAGGGTTACAGTAACTGGAGAATGCTTAAAGATGCTTAAAGATGCTACAT 1204
QY	950 GACGCCCTGGACAGGTGGTAAAGATPACAGTGTGATAAAGATAGCACAAATGTTGA 1009
DB	1203 AGAGCCTTGGACACTGCTGTTAAGCATGCTGTTAAGAACATACATGTTGA 1144
QY	1010 AGCTTGGAGGAGCTGAGACTTGCACCTATGACCTATGACCTAAATGGAAATTAGCTGG 1069
DB	1143 AGTGTGTTGCTGTTGTCATGATGTTGAATAGACATACATGTTGA 1084
QY	1070 AACGAAACTCTGACTTGGCTGAAACTAACAGAACGCTTGGAAATTAGCTGG 1129
DB	1083 AAAATACTCTGTTGGCTGAAATAGACAGCGCTTGGAAATTAGCTGG 1024
QY	1130 TAGTGTAGCTTATCAAAGGAGCCACAGAGACGTTAACAAATGAAACT 1189
DB	1023 CGAGGTGGGGTAGTTAACATGAGCCACAGACATTAAGCAATGCT 964
QY	1190 TGGCATGGAGGAGCATTATGACACAGCGCTGCTGTGAGAAGGGTTCTGG 1249
DB	963 TTGATGTAGGAGGAGCATTATGACACAGCGCTGCTGTGAGAAGGGTTCTGG 904
QY	1250 TGTGTCAGGCACTTATGGTTATGAAAGTAGGCTCTGAGCTTGGCGCA 1309
DB	903 TTGTCGATACGCTCTTAAAGCAGCATGAGCTTGGATAAACTTCAAGAGCGA 844
QY	1310 TGATGTCAGGAGGAGCATTATGACACAGCGCTGCTGTGAGAAGGGTTCTGG 1369
DB	843 CATTCAACAGGATTACATCGTCGGCGGCCCTGAGACCCATCGTC 784
QY	1370 TTAATAGTGGTAGGAGGCTGCTGTGAGCTTGGAAAGAACGCTTCAG 1429
DB	783 GCCATGGAGGATGAGTAACTGGTCAATCTGTCAGTATCTGGTCAAAAGTGG 724
QY	1430 AACAGGATTTAGTCACAGCTGAGTGGTGATGATTAACAGGAATCARTGA 1489
DB	723 TACAGGATTAAAGCAGCAGACTCAATGGTAATATGTTGAGAGGAACTGTGA 664
QY	1490 CCCTGTCAGGATCACAGATCAAGCTTCACAATACAGCTTCAGGCTCAG 376
RESULT	5 AY108560
LOCUS	AY108560
DEFINITION	mRNA sequence.
ACCESSION	AY108560
VERSION	AY108560.1
KEYWORDS	HTC, Zea mays.
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; clade; Paniicidae; Andropogoneae; Zea.
ORGANISM	Hanley, C.F., Dolan, N., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
REFERENCE	1. (bases 1 to 2143) 2. (bases 1 to 2143)
AUTHORS	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Ovago Probes
JOURNAL	Unpublished (2002)
REFERENCE	3. (bases 1 to 2143)
AUTHORS	Cole, E.C.
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
FEATURES	Direct Submission
SOURCE	/organism="Zea mays" /db_xref="MaizeDB:638266" /clone_id="PO010434"
BASE COUNT	546 a 546 c 598 g 505 t
ORIGIN	Query Match 23.1%; Score 383.6; DB 11; Length 2143; Best Local Similarity 54.0%; Pred. No. 7.5e-96; 0; Mismatches 734; Indels 16; Gaps 4; Matches 880; Conservative
QY	18 GAAAAGAAATCAATTTCAGAGATGGGGCTCTGCATGGTGGGGAGCTGTGATG 77
DB	274 GCGAACGAGATGCCCTTGACAGGAGGGCTCAGAGCGCCCTCAGGCCGGCAGAG 333
QY	78 TTAGCAGATCCGTCAGAATGACCTCTGGTCTAAAGGGCGAAATGTTCTGTGAAA 137
DB	334 CTCGCGCCGCGCTGGCGCACCTGGACCGAGGAGGAGTCTCTGGTAG 393
QY	138 GCTTGGTAGCTTAACTACAGGGAACTATGCTAAAGATGATTAA 197
DB	394 ...TTTGAAACCCCAAGGGTCAATGAGTGGAGTCAATGGCCGCTATAGGCT 450
QY	198 GAAGTCATTTGAAACATGGAGCAATATGGTGTGAGTGGCTCTAACACAT 257
DB	451 GCGATCCCTGAGGATGCTGGCTTCCTGTTGAGTGGCTGAGGAGGAGGAG 510
QY	258 GATATGCGTGTGATGGGACAC-TATGCAACAGTTGACACAGCAATGCTGA 316
DB	511 GACTCGCTGTGTTGAGAACACAACTGCGCTCTGTTCTGGAGGACATCAATT 570
QY	317 AGGATAAAAGTGTACAGCAGGTGTTGCTTCATGTTGAGTGGCTGAGGAGAAC 376



	SOURCE	ORGANISM	zea mays.
Qy	658 ACCATTAACTAACCGATAAAGTCACAACATCCAGACATTGCAACTAC	Zea mays	
Db	203 ACCRTTTCATCATGACAGAACTCAACATGATTCCTCCAGCT	Bikaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.	
Qy	7118 TTAGGAAAGTTCTAACCCACGGTCATTACCATATTGAGATGTTGGG	REFERENCE 1 (bases 1 to 1387)	
Db	263 TAGATTCTATCAGAACTGGCAAGCCTCTCATGTGAGGAGG	AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsett, M.S., Arthur, L.W., Hanafey, M., Morgante, M and Tingey, S.V.	
Qy	778 AACACTTCACCCCTGCTGAAAGATGCTGACTTCATGTTGTTGCA	TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overo Probes	
Db	323 ATGCCTGTCATGCTTGTACGTCAGCTGCTGTCAGGATGTC	JOURNAL Unpublished (2002)	
Qy	838 AAGCCTACAGATGTTGGTGAACCTGTTGAGACATGCTCTGTC	2 (bases 1 to 1387)	
Db	383 AACGCCCTGAGTTAGGAAATAGGACACATCTGAGATGATGAG	COE, E.C.	
Qy	898 GGGCACAGCTGCTAGATCAGTGCTAAGATAGCACAGTATG	382	
Db	443 GAGGAGGTTAGGAGGACGGGTCTGATCTGCAAGTCAATGAC	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA	
Qy	958 TTGACACGCTCTAGATCAGTGCTAAGATAGCACAGTATG	502	
Db	503 TTGGACTCTAACAGAACGACTGATCCCTGATGATCTACATGAG	562	
Qy	1018 GAGGETCAGAGCTATGCTAACCGPATGCTTAATCCAAATTGAA	/clone="PEO123570"; /clone_id="MaizeDB:637188"; /db_xref="taxon:577"; /db_xref="taxon:577"; /clone="PEO123570"; /clone_id="Maize Mapping Project/DuPont Cornsensus Library"; /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"	
Db	563 GTGACAAACAGGAGATAGTGGAGAGGTGCCAACAGCTAGAACAGCA	1077	
Qy	1078 CTTCGACTGTGACGGTGAAGAACTACAGAACAGCTTGGGA	622	
Db	623 CTGGTTTTCGACAAAGAAAGCCCAAGGGTTTCTACTTCTGAGCTG	1137	
Qy	1138 CTGTTAACTAGAGCTCCACAGAGACGCTTAAAGAAATGAACTTG	1197	
Db	683 CTGRACTCAAGATGGTGGCACTGAGCTGAACTGTTGGGAA	742	
Qy	1198 AGATGCTTAATGCTACAGTGCGACGGTTCAGAGGATTTGGGA	1257	
Db	743 CAGATGCTTAATGCTACAGGCTGCGTGGAGGGCATTGCGAGG	802	
Qy	1258 CAGGACTTATGCTTATGAAAGTAGTGACCTTGACGTTGACG	1314	
Db	803 TTGCCCTCTTATGCCAACGAGCTGACAGATAGCACAAACGGAA	862	
Qy	1315 CTACTGGACGTTACATGCTGCGCTAGAACGGCTGACGCTTAA	1374	
Db	863 AGATGGGTCAAATTCTCAGAACTCTTGGAGCTCCTTGACCA	922	
Qy	1375 ATGGCTGTTAGAACGGCTCCGTGTTGATGACAGTGA	--AAAAGACGCTCAGAA 1431.	
Db	923 ATGGTGGCATGATGGAGCTATGCTAGTGGAGGTGATGAA	982	
Qy	1432 CAGGTTATGCTCACAGGTTGCTGTTGATGATTAACGGAACTGT	GACCCTGAC 1491.	
Db	983 TGGCTTGTGAGCAGGGAGTAGTGACATGATGAACTGCTCAG	CATCACT 1042	
Qy	1492 CTGCAAAAGTACAGAACGGCTTCAAAGACACTCTGACCTT	TTGTTGAC 1551.	
Db	1043 CGGTGAAGTGTGACGGCACTGACTTCAGACGCTGAC 1102.		
Qy	1552 CARCAGAGCAGTGTGTTCTATAACCTGAGC	1585	
Db	1103 CCAGGGAGCCCTCTCGGAGCTCCGGCAGC	1136	
RESULT 7	AY108518	AY108518	1387 bp mRNA linear
LOCUS	2ea	mRNA	HTC 25-MAY-2002
DEFINITION	2ea	mayS	
ACCESSION	AY108518	PC0123570	
VERSION	AY108518.1	GI:21211595	
KEYWORDS	HTC.		

QY	1108	ACGTTGGCAAATTAGCTGCGGTAGCTTATCAAGTAGGAGCTCCAACAGAGA	1167	JOURNAL	Submitted (09-SPR-2000). Genoscope - Centre National de Séquenage, 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : secrétariat@genoscope.cnrs.fr) . Web : <a href="http://www.genoscope.cnrs.fr">www.genoscope.cnrs.fr</a>		
Db	554	AGAGAACTAACGCTTGCGGGGTTGCTTAAGGTGGACTGCAACTGAGA	613	COMMENT	This GS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces cerevisiae</i> , <i>Saccharomyces bayanus</i> var. <i>varatum</i> , <i>Saccharomyces exiguus</i> , <i>Saccharomyces servazzii</i> , <i>Zygosaccharomyces rouxii</i> , <i>Saccharomyces kluveri</i> , <i>Kluyveromyces lactic</i> var. <i>lactic</i> , <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> , <i>Ricchia angusta</i> , <i>Debaromyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.		
QY	1168	CGCTTAAACAAATGAACTTCGTTAGGTGCTTAATGCACTGAGCG	1227	FEATURES	Location/Qualifiers		
Db	614	CAGACCTTGAGGCCGCGACTTAAATGAACTTGTGAGGTCAGCTTGCAGTA	673	source	1. -887 /organism="Kluyveromyces lactis" /strain="CILB 210" /variety="lactis" /db_xref="taxon:28985" /clone_id="B04AB027507" <4...>887 <4...>887 /note="similar to <i>Saccharomyces cerevisiae</i> ORF YLR259c [ HSP60 ; heat shock protein - chaperone, mitochondrial ]" /evidence="not experimental"		
QY	1228	TGGAAGAGGTATCGTGCCTGGTGAACAGACGCTTAAATGCTTAA	1278	BASE COUNT	256 a 163 c 216 g 252 t		
Db	674	TGAGAGGGCATGTCAGGAGCTGAGCTGAGGTCAGCTTGCAGTC	733	ORIGIN	Query Match 15.8%; Score 263.2; DB 17; Length 887: Best Local Similarity 58.7%; Pred. No. 2.4e-62; Mismatches 343; Indels 4; Gaps 2; Matches 493; Conservative 0; MisMatches 343; Indels 4; Gaps 2;		
QY	1279	AAAGTAGGACGCTCTGACTTGAGCTGGGGATGATGCTACTGGAG	1338	QY	21 RAAAATCAATTAGCATGAGATCGCGGTGCTGCAGAGTTGATCTTA 80 Db 914 TCGGAACTCTTGAGGCTGGTGTGATGCGCTCCAGGTGCGTC 973 QY 1518 CAATGAGCTCTGATGACTCTTATTTGACACAGAGGAGTGTGCTATAAA 1577 Db 945 TGGTGTGATGATTAACAGGATCATGACCTCTTAAAGTAAACGATCAGC 1517 QY 1578 CCTGACCGCTACGCCAGGCCGACATCCACCG 1615 Db 1034 CCAAAGCCGAGCCTAACGGCAGGCCGAGGG 1071	QY	25 AAAGATAAAGTTGGTTGAAGGTGAGCTGCCTGTTAAGGGTGTGAAAGCT 140 Db 81 CGAGATCCTCAAGTACCGTGTGCTTAAAGGTTGAAAGCTTGTGCAACCA 84 Db 85 GCGGAAGCTTGTGCTCAGTTGGTCCAAAGGTTGAAAGGTGAAAGCTTGTGCAACCA 144 QY 141 TGGTCTCTTAACTACTAATGACGGGAACTATGCTAACAGATGATTAA 200 Db 145 TTGGCCCTCAAAAGATCACCRASGATGTTCTGTTACGTGCTAGAGCTTGGAA 204 QY 201 GATCATTTGAAACATGGGACAATTTGTTGTTGAGTGTGCTGCTCTAAACCAAGAT 260 Db 205 GATAGTCGAAACATGGGCTTACAGAGTGTCTTCAGAAGCTTCAGAACAGCA 264 QY 261 ATTCGTTGATGGGACGACTGCAACAGTTGACACAGCCATTGTCATGAGGA 320 Db 265 GCTGCCGTTACGCTTACCTCTCTGTTAGGCTTCTGCTACGATTC 324 QY 321 CTAAATATGAGCAGGAGCTTACATGATGTCATGCTGAGCAGTGAACAGCA 380 Db 325 GTTAAGATGTTGCAAGTTGACCCATTGTTGAGAGAGGTACTCAAGCTGCT 384 QY 381 ACAGCACAGCTGTGAGCTTGAAGCCATTGTCACCTGTATCTGGCAAGGAGCT 440 Db 385 GTGAAATAATTTCTTACATGAGCAGAACAGAACACCTTGTGCAA 444 QY 441 ATTCGTCAGTGTGCAAGTACATGCTGAAAGTAGGAGGTATATCTCA 497 Db 445 ATGGCTCAAGTGGCACTATTTCTGCCACCGGGGTCTCAGTTGTTGCT 504 QY 498 GAAGCTATGGCTGGGAAAGTGTGTTGATACATGAGAACTCTCAAGGATG 557 Db 505 TCAGCTTGAAGATGTTGAGAGGTCTCATCATGAGAGGGTCAACCTG 564 QY 558 GAAACGACTTGAGTGTGAGGCTGAGTGTGCTTCAATAC 617 Db 565 GAAGTGTGAGGAGCTGAGGATGATGAGCTGACCGGTGTTCTTCATAC 624 QY 618 ATGGTCAAGACATGAAATGGTGCAGACCTTATCTAACTCAGC 677
REFERENCE	1 (bases 1 to 887)						
AUTHORS	Souciet, J. L., Aigle, M., Artiguane, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de Montigny, J., Dujon, B., burress, P., Lepingle, A., Llorente, B., Malpertuy, A., Neveuville, C., Olier, Kalioperopoulos, O., Peltier, S., Saurin, W., Tekka, F., Toffano-Noguel, C., Wesolowski-Louvel, M., Wincker, P., and Weissenbach, J.						
TITLE	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies						
JOURNAL	FEMS Lett. 247 (1), 3-12 (2000)						
MEDLINE	2058471						
PUBMED	11152876						
REFERENCE	2 (bases 1 to 887)						
AUTHORS	Boilot, N., Fukuhara, M., Toffano-Noguel, C., Artiguane, F., Baudouin, N., Guyenot, G., Lemaitre, M., Marmisse, R., Montrozier, R., Robert, C., Trémier, M., Wincker, P., and Wesolowski-Louvel, M.						
TITLE	Genomic exploration of the hemiascomycetous yeasts: 11.						
JOURNAL	FEMS Lett. 247 (1), 66-70 (2000)						
MEDLINE	2058471						
PUBMED	11152886						
REFERENCE	3 (bases 1 to 887)						
AUTHORS	Genoscope						
TITLE	Direct Submission						

Db	625	TTATACCGAGCCTAACTGGTAAGTGGATTGAAACCTTGATCTATGAGT	684	Oy	198	GAACATCATTTGAAACATGGGACCAAATGGGTCAGTGCTTAAACCAAT	257
Oy	678	GATAAAAAGTGTCAACAACTCCAAAGCATTTGCAACTTGTGAGGAGTCTTAAACC	737	Db	302	AACATAAATCAGAACATGACCTAACTTGTCAGATGTTGCCATACACAT	361
Db	685	GAAGAGAGATCCTCCTAACCCGGATATCTGCCTCTTGGATGTCAAACCAACC	744	Oy	258	GATTTGCTGTGAGGGACGACTACTGCAAGTGTTCACAAACCCATGTGAGA	317
Oy	738	AACCTCCATTACTCATTTGAGATGATGTTGGATGTCAGACTCCACCTTGTC	797	Db	362	GAAGAACCTGGGGTGCACTTACACTGCTACTGACTGAGCCTATGAGA	421
Db	745	AGAAGACCTGTGATCATCGCCGAGATATGATGCG-ACTTTGGCTGCTGTAT	803	Oy	318	GGCTAAATGTCAGCAGCGATTGTCATGTTGCTCAARAGCCCGGATTGTTGAT	377
Oy	798	TGAACTAGATCGUGGACTTCATGTTGCTCTCAARAGCCCGGATTGTTGAT	857	Db	422	GGCTCCAGAAGATAGCAAGCTTATCCAGTGGAAATGGAGGTGATGTTA	481
Db	804	TGAACTAGATCGUGGACTTCATGTTGCTCTCAARAGCCCGGATTGTTGAT	863	Oy	378	GCAACACGACAGCTGTTGACCCCTGAACCTATCTGGCAAGGAA	437
<b>RESULT 9</b>							
LOCUS	BM799922	1090 bp mRNA linear EST 05-MAR-2002		Qy	438	GCTTTGCTGAGGCGCAGTGTGTTACATCACCTGAAAG--TTGAGGTTATC	494
DEFINITION	ACBNCDRT-6417164 NIH_MGC_67	Homo sapiens cDNA clone IMAGE:5492101		Db	542	GAATTGACAGGTTGCTACATTGAAATTGCAATATC	601
REFERENCE	5', mRNA sequence.			Qy	495	TGAGACCTGGCGTGGACCATGTTGATGATACGAACTCTCAGG	554
AUTHORS	(bases 1 to 1090)			Db	602	TCTGATCATGAAAGTGGAGAAGGGTGCATCAGTAAAGGTGAAAC	661
VERSION	BM799922.1	GI:19116745		Qy	555	ATGGAAACAGACTGTGGTGAAGCAGTCACTCAGCTTGAAAG--TTGAGGTTATC	614
KEYWORDS	EST, human.			Db	662	CCTGATGATGATGAAATTGAGGCTTCTGAAACGAGAAATTGCAATATC	721
SOURCE	Homo sapiens			Qy	615	TACATGTCACAGCAGTAAATGTTGAGAAGTGGAGAAGGGTGCATCAGTAAAGGTGAAAC	674
ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			Db	722	TACTTTTATGATCATAAAAGTCAGTCACTCAGCTTGAAAGTGGTACCTGTC	781
JOURNAL	Unpublished (1999)			Qy	675	ACGGATTTAAACGTCGAACATCAGACATGAGGCTGAGTGTGAGGCTATTCATA	734
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgsaps-r@mail.nih.gov			Db	782	AGTGAAGAAGAAATTCTAGTATCCAGTCATGTTGACTTGCTGAAATGCCATGT	841
TISSUE	Procurement: ATCC			Qy	735	ACCAACGGTCATTCATGAGTGTGGAGCACTTCACCCCT	794
PREPARATION	Life Technologies, Inc.			Db	842	CACCGPAAAGCTTGTCTCATATGCTGAGTGTGGAGAAGCTTAAGTAC	901
CDNA LIBRARY	Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			Qy	795	GTCTTACAGATTCCTGGACTCTCATGGTGTGGTCAAGGCCAGATTTG	854
DNA SEQUENCING	Agencourt Bioscience Corporation			Db	902	GTCTTACAGATTCCTGGACTCTCATGGTGTGGTCAAGGCCAGATTTG	961
CLONE DISTRIBUTION	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov/plate/LLNL2113. row: k column: 14			Qy	855	GATCGCGTAAAGCTTGTCTGGAGATGCTCTCTGGAGGGTGTACATGTTACA	914
PLATE	LLNL2113. row: k column: 14			Db	962	GACATAGAAAGACCGACCTAAAGATAGCTGCTATGCTACTGGGGCCAAAGTTG	1021
<b>High quality sequence stop: 733.</b>							
<b>Location/Qualifiers</b>							
SOURCE	1..1090			Qy	915	GAGGACTCTGGACTCTGGTGTGGTCAAGGCCAGATTTG	928
<b>/organism="Homo sapiens"</b>							
<b>/db_xref="taxon:9606"</b>							
<b>/clone="IMAGE:5492101"</b>							
<b>/clone_id="NH_MGC_67"</b>							
<b>/tissue_type="retinoblastoma"</b>							
<b>/lab_host="DHLOB" (phage-resistant)"</b>							
<b>/note="Oran: eye; Vector: pCMV-SPORT6; Site: J: NotI; Site: 2: SAI; Cloned unidirectionally; Primer: Oligo dT Average insert size 1.75 kb. Library constructed by Life Technologies."</b>							
BASE COUNT	332	a 209 C 274 G 275 T		RESULT 10			
ORIGIN				LOCUS	BP27584		
Query Match	15.81;	Score 262.8; DB 14; Length 1090;		DEFINITION	BP27584		
Best Local Similarity	56.24;	Pred. No. 3. 6e-62;		ACCESSION	BP27584	Gossypium arboreum	
Matches	514;	Conservative 0; Mismatches 397; Indels 3; Gaps 1;		VERSION	BP27584.1	cDNA clone GA_Ebo02423f, mRNA sequence.	
Oy	1B	GCAAGAGAAATCAATTTGCGAGATGGCGCTGGCGCATGTCGCGCAGCTGATG	77	KEY WORDS			
Db	122	GCCAAAGATGATTAATTTGGCGAGATGCCAGCTTATGTCAGGTGTTAGACCT	181	EST			
Oy	7B	TTCAGCATGTCGCAAGTAGACGAGCTGGCTTAAAGGGCGATGTGCTTGAA	137	SOURCE			
Db	182	TTCAGCATGTCGCGCTTACATGGCGCAAGGGAGAGACGTGTTAGCG	241	ORGANISM			
Oy	138	GCTTGTGCTCTCTTAATTACTATGACGGGTACACATGTCAGAGATGCGTTA	197	Bivalvia; Virodiplopoda; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.			
Db	242	AGTTGGGAAGTCCAAAGTAGACAAAGATGGTGACTGTCAGCTAACATTGACTA	301	REFERENCE			
				AUTHORS			
				TITLE		An integrated analysis of the genetics, development, and evolution of the cotton fiber	
				JOURNAL		unpublished (2000)	

COMMENT	CONTACT: Wing RA Clemson University Genomics Institute 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwling@clemson.edu Seq. Primer: TATAGGACCTATATGG High quality sequence stop: 716. Location/Qualifiers
FEATURES	SOURCE
BASE COUNT	253 a 157 c 219 g 245 t 4 others
ORIGIN	/organism="Gossypium arboreum" '/strain="AKA" '/cultivar="B-00" '/db_xref="taxon:29729" '/clone_id="Ebo024623f" '/clone_lid="Ecossypium arboreum 7-10 dpa fiber library" '/issue_type="Fibers isolated from bolls harvested 7-10 dpa" '/lab_host="E. coli" '/note="Vector: PBK-CMV; Site 1: EcoRI; site 2: XbaI" '/note="Vector: PBK-CMV; Site 1: EcoRI; site 2: XbaI"
RESULT	11
ALN18632	ALL18632 LTI_NFL01_NBCL Homo sapiens mRNA linear EST 13-FEB-2001
LOCUS	AL518632 LTI_NFL01_NBCL Homo sapiens mRNA clone CSODA09Y115 5
DEFINITION	PRIM, mRNA sequence.
AUTHORS	LJ W B Gruber C Jeejee J and Polyes D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope Genoscope - Centre de Séquençage BP 191 91005 Evry cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES	Location/Qualifiers
SOURCE	/organism="Homo sapiens" '/db_xref="taxon:9606" '/clone_id="CSODA09Y115" '/clone_lid="LTI_NFL01_NBCL" '/sex="male" '/tissue_type="neuroblastoma cells" '/lab_host="DH10B" '/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-digested primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RI sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax : (1) 301 610 8371 Email : http://fulllength.invitrogen.com"
BASE COUNT	311 a 195 c 259 g 266 t 4 others
ORIGIN	/organism="Homo sapiens" '/db_xref="taxon:9606" '/clone_id="LTI_NFL01_NBCL" '/clone_lid="CSODA09Y115" '/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-digested primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RI sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax : (1) 301 610 8371 Email : http://fulllength.invitrogen.com"
Query Match	15.5%; Score 257.2; DB 9; Length 1035;
Best Local Similarity	56.3%; Pred. No. 1_3e-60;
Matches	500; Conservative 1; Mismatches 384; Indels 3; Gaps 1;
Db	448 CGAGTTCAAACCTACTGTGTTGGTGGCGGAACTTCGCTG 507
Oy	961 GACAGGCTCTAAGATAATCGATGATAAGATACAGCATGTTAAGA 1020
Db	508 GATGCGCAAGAGGTGACATACAGATGCTGCTGCTGCTGCTG 567
Oy	1031 GTTCAGAACCTATGCTAACCGTATCAGTATTACCCATTGAAACAACTT 1080
Db	568 CHAAGATGAGATACANACTAGGTGGCACAACTTAAGAAAGCTGAGATT 627
Oy	1081 CGGACTTGTGACCTGAAGAACTTCAAGAATGCTGGATGCTGGTAGTG 1140
Db	628 CGTCATATGATGAGAAATTGCGAGAGGATGCCAACTATCTGTGCTG 687
Oy	1141 TATCAAGTAGGAGTCACAGAGCACTTAAAGAAATGCTGAGTGCCTTAACCAAT 257
Db	688 TCATTAAGGTGGGGCTTACACAGACAGTCACTGGTTCTAACCTACGGATGGAG 747
Oy	1201 ATGCTCTTAATGCTACAGTGGCAGCGGTGAGAAGGTATGCTGCTGCTG 1260
Db	748 ATGCAAAAGATGCTACATTGTCGCTAGNGANGTATTGCGCTGGTGTGCTG 807
Oy	1261 CACTAT 1268
Db	808 CCTTAGTT 815

	FEATURES	LOCATION/QUALIFIERS
	SOURCE	1. .977 /organism="Zea mays" /cultivar="C0128"; /db_xref="taxon:577"; /clone="Zm04_04909"; /tissue_type="Leaf, crown" /notes="Vector: Bluescript SK-/XbaI-EcoRI; Site_1: Eco RI; Site_2: Xba I; Lower temperature 50 C / hour from 22 to 120C; bring to 50 in 1 hour from 120C. Leave at 50C 2 days photoperiod 16 hours. Light intensity was 125 U.E.-1 library prepared by in vivo mass excision from amplified library";
Db	296 AAAGATAAAATACAAAACATGGGACTTAACTTGTCAAGATGTTGCCAATACACAAT 355	
Oy	258 GATAATGCGCTGATGGGAGACTACTGCACAGTTGACACAGGCGATGTTGATGAA 317	
Db	356 GAAGAGCGGGGGATGCACTACAGCAGTCAGTGTACTGCGACCTCTGAGCACAGA 415	
Oy	318 GGACTTAAAGAATGCGACAGCGCTGTAATCCATGGTATCCCTCGGGATGAA 377	
Db	416 GGCTTCGAGAGATTAGCAGAACGGTGCTAACAGTGGAAATCAGTGGAAAGGGGG 475	
Oy	378 GCAACAGACAGCAGCTGTTGAACTGAAGCTGAAGCTCACTGCACTGTTGAGAA 437	
Db	476 GCTGTGATGCTGTAATGCTGACTTAAAGCAGTCTAACCTGTGACCCCTRA 535	
Oy	438 GCTATGCTCAGCTGCTCAGTCACTGCACTGAAAGGCAATGGGACAAAGAAATGGCAATC 595	
Db	536 GAAATTGCCACAGGTTGCTGAGTTCTGAAAGGCAACAGAAATGGCAATC 595	
Oy	495 TCAGAGCTATGGGGTGGCCACAGTGGTTTACCTCGAGAAATCTCGAGGT 554	
Db	596 TCTGATGCTGATGAAAGAATGTTGAGAAGGGTGTACATCACTAAGGGAANCA 655	
Oy	555 ATGGAACAGACTGAGTGTGAGGCAATTGAGGCAATGGTGTACCTCTCAA 614	
Db	656 CTGATGTTGATGTTGAGTATGAGGATCTGGGGTGTACCTCTTGTAA 715	
Oy	615 TACATGGCAAGCAAGTGAAGAAGAAATGGTGTGAGCTTGAAACCATTTATTTAA 715	
Db	716 TACTTTTATACATCAAAAGTGTGAAATGTTGAGGATCTGAGGTTGCTGTTG 775	
Oy	675 ACGGATAAAAGTGTCAACATCCAAAGCATTTGGCACTAATGAGGTCTTAA 734	
Db	776 AGTGAAGAAATTCAGTATGGCTCATGTTGACTCTTGTGAATGCGAACT 835	
Oy	735 ACCACACGGCTTCACTACTATTTGCGATGAGTGTGAGTGTGAGCTTCACCTT 794	
Db	836 CACCGTAGCCATTGCTATATCCTGAGAGTGTGAGGAGTGTGAGGAGCTTAA 895	
Oy	795 GCTCTGACAGATCTGTTGACTTCAATGCGCTGCTCAAGGGCGAGGTTGGT 854	
Db	896 GTCTTGATGCTAAAGTTGCTCGAGTGTGCGACTCAGCTCCAGGGTTGG 595	
Oy	855 GATCGTGTAGTGTAGCTGTTGAGACATGTGTTGAGTGTGAGGTGT 902	
Db	956 TGACATATAGAGACCTTAAAGATGTTGAGTGTGAGTGTGAGGTGT 1003	
RESULT 1 2		
BE321293	BC321293 977 bp mRNA linear EST 27-FEB-2001	
DEFINITION	Zm04_04909_R Zm04_AAFC_ECORC_cold_stressed_maize_seedlings_Zea_mays	
ACCESSION	Zm04_04909 mRNA sequence.	
VERSTON	BC321293	
KEYWORDS	EST.	
SOURCE	Zea mays.	
ORGANISM	Zea mays	
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. (bases 1 to 977)		
REFERENCE	Singh,J.A., Wakui,R., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprot,D. and Tinker,N.A., 1991. Expressed Sequence Tags from Cold-Stressed Maize Seedlings. Unpublished (2001)	
AUTHORS	Contact: Singh,J.A. Eastern Cereal and Oilseed Research Centre Agriculture and Agri-Food Canada K.W. Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A 0C6, Canada Tel: (613) 759-1662 Fax: (613) 759-1701 Email: singhj@em.agr.ca.	
COMMENT		

RESULT 13 AL532233 LOCUS AL532233 DEFINITION AL532233_UTI_NFL001_NBC4 PRIMER mRNA sequence.	988 bp mRNA linear EST 13-FEB-2001	Db 475 GCTGTGATGCTGTAATGTGAACTAAAGCGTAAACCTGGCCACCGTGA 534
REFERENCE Li, W.B.; Gruber,C.; Jesse,J. and Polaves,D. AUTHORS Li, W.B.; Gruber,C.; Jesse,J. and Polaves,D. TITLE Full-length cDNA libraries and normalization JOURNAL Unpublished (2001) COMMENT Contact: Genoscope	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 988) /note="vector: pmwsp6, site_1: NotI: 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pmwsp6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 http://fulllength.invitrogen.com"	Qy 438 GCTATGCTCAGTCGCTGAGTATCATCGCTCTGAAAG---TUGGAGCTTATC 494 Db 535 GAARTGCCAGSTGTCAGATTCTGCACACGGACAGAATGGCATATCATC 594 Qy 495 TCGAGCTATGGCGTGCGCAGATGTGTTACCATGCAATCTCCAGGT 554
FEATURES SOURCE source	Homo sapiens Email: seeref.genoscope.cns.fr, Web : www.genoscope.cns.fr.	Db 595 TCGANGCAGTGAAGAACAGTTGGAGAAGCGTCACTCACGTAAGGATGGAAACK 654
BASE COUNT	306 a 188 c 242 g 251 t 1 others	Qy 555 CTGATGATGATGAAATTAGAATTTGAGGCTGAAATTGACCGTGTACCTCAA 674 Db 655 TCGATGATGATGAAATTAGAATTTGAGGCTGAAATTGACCGTGTACCTCAA 714
ORIGIN	Query Match 15.3%; Score 253.4; DB 9; Length 988; Best Local Similarity 57.1%; Pred. No. 1; 5e-59; Matches 500; Conservative 0; Mismatches 371; Indels 4; Gaps 2; Qy 18 GCAMAGAACATCATTTCGCAAGTGGCGTGGCCATGGGGAGTTGATG 77 Db 115 GCAAAGATGTCATAATTGTCGACATGCCGAGCTTATGTTCAAGTGTAGACCT 174 Qy 78 TTACAGATACCGCAAGTAACTGTCGTTGCTTAAGGGCGRATCTGTCTGARAA 137 Db 175 TTACGCGATGCTGCGCTTACAATGGCCAAKGGAGAACAGGATATGACCG 234 Qy 138 GCTTTGTTCTCTTAACTACTATGACGGGTTACATGCTAAAGAGATGAAAT 197 Db 235 ATGGGAAACTCCAAAGTACAAAGAATGTTGAGCTGTGCAAGTCAATGCTA 294 Qy 198 GAAGATCATTGAAACATGGAGCAAAATGTTGCTGACTGCTCTAAACCAT 257 Db 295 AACATAAAATCACAAACATGGAGCTAACTGTGTCAGATGTTGCAATACAAAT 354 Qy 258 GATATGCTGTTGAGGAGCTACTGCAACAGTGTGACRAAGCCATGTCTGAA 317 Db 355 GAGAGCTGGGGAGGCTACCCATGCTGAGCTGCTATAGCCAGGAA 414 Qy 318 GGACTAATAATGTCAGCAGCTGCTAACTCAATGGATCGTGGAGCATGARAA 377 Db 415 GGCTTCGAGAGATAGAAAGTGTGCTTAATCGTGAATCGAGGAGGTGATGTTA 474 Qy 378 GCAACAGCAACAGCTGTTGAGACCTGTCACACTATGTGCGAAGGAA 437	Qy 615 TACATGGTCACAGACATGAAATGTCAGCTGAAACCCATTCTTAACT 674 Db 715 TACTTATTAATACATCAAAGTCAGATGTGATGTCAGATGCTATGTCAGTC 774 Qy 675 AGGATTAAGAACAGTCAACATCCAGACTTTCGCACACTATGTCGAACT 834 Db 775 ATGAAAGAAATTCATGTCAGCTGTCAGTGTGTTGATGTTGCAATGCT 834 Qy 735 ACCACCGTCATCATCTCATATGCGATATGGGGGGAGCACTTCACCCCT 794 Db 835 CACCGCAACTCTTGTGCAATGCGAGATGTGATGGAGNGCTCAATGTCAC 894 Qy 795 GCTGCAACAGATGTCAGCTGAACTTGTGACTTGTAACTGTTGTTGTC 854 Db 895 GCTTGCAATGGCTAAAGGTGGCTTCAGSTTGCAGCAGCTCCAGGTTGGT 954 Qy 855 GATGCGCAACACTATGCTGAGACATCTAT 889 Db 955 GACAATAG AAAGCAGCTAAAGATGATGGCT 988
BASE COUNT	306 a 188 c 242 g 251 t 1 others	RESULT 14 AL51262 LOCUS AL51262_UTI_NFL006_PL2 DEFINITION AL51262_UTI_NFL006_PL2 Homo sapiens cDNA clone CL0BB0162A04 5 ACCESSION AL51262 VERSION AL51262.1 KEYWORDS EST. ORGANISM Homo sapiens Human. Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 955) AUTHORS Li, W.B.; Gruber,C.; Jesse,J. and Polaves,D. TITLE Full-length cDNA libraries and normalization JOURNAL Unpublished (2001) COMMENT Contact: Genoscope Genoscope - Centre National de Séquençage BP 191 91006 EVRY cedex - France Email: seeref.genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES SOURCE source	/note="vector: pmwsp6, site_1: NotI: 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pmwsp6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"	Db 475 GCTGTGATGCTGTAATGTGAACTAAAGCGTAAACCTGGCCACCGTGA 534 Qy 438 GCTATGCTCAGTCGCTGAGTATCATCGCTCTGAAAG---TUGGAGCTTATC 494 Db 535 GAARTGCCAGSTGTCAGATTCTGCACACGGACAGAATGGCATATCATC 594 Qy 495 TCGAGCTATGGCGTGCGCAGATGTGTTACCATGCAATCTCCAGGT 554
BASE COUNT	288 a 181 c 236 g 247 t 3 others	Db 595 TCGANGCAGTGAAGAACAGTTGGAGAAGCGTCACTCACGTAAGGATGGAAACK 654

VERSION	AL515579.1	GT	1:12779072
KEYWORDS	Query Match; Best Local Similarity; Matches 480; Conservative; Definition; ACCESSION		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	(bases 1 to 1017)		
AUTHORS	Liu, W.B., Gruber, C., Jesse, J. and Polayes, D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Genoscope - Centre National de Séquençage BP 191, 91006 Evry cedex - France Email: <a href="mailto:segref@genoscope.cnrs.fr">segref@genoscope.cnrs.fr</a> , Web : <a href="http://www.genoscope.cnrs.fr">www.genoscope.cnrs.fr</a>		
FEATURES	Location/Qualifiers		
SOURCE	.1..1017 /organism="Homo sapiens" /db_xref="txion_9606" /clone="CS000010D0" /clone_id="LTL-INFULL.NBCI" /sex="male" /tissue_type="neuroblastoma cells" /lab_host="B10B" /note="Organ: brain; Vector: PCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched double-stranded cDNA was digested with NotI and cloned into the Not I and Eco RV sites of the PCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA. Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : <a href="http://fulllength.invitrogen.com">http://fulllength.invitrogen.com</a> "		
BASE COUNT	308 a 191 c 255 g 261 t 2 others		
ORIGIN			
Query Match	15.0%; Score 249.6; DB 9; Length 1017;		
Best Local Similarity	56.8%; Pred. No. 1.7e-8;		
Matches	478; Conservative 1; Mismatches 360; Indels 3; Gaps 1;		
QY	18 GCAAAAGAACATTTCACAGATGGCGCGCTCCATTGGGCCGGGGTGTATG 77		
Db	116 GCCAAAATGTAATTTGTGCAGATGTCGCAGGCCATTAGTCCTCAGGGTACCTT 175		
QY	78 TTACAGATACCGTCAAATGGAATGTTGACGCTTGAAACCCATTATCTTAC 674		
Db	176 TTACCGATGCTGTCGCCATTACATTGGGCCAAAGGAAAGCAGGTGATTTGACAG 235		
QY	138 GCTTGTGTTCTCCCTTAATCTACTAATGCGGGGTAACTCTCTAAAGAGATCGATA 197		
Db	236 AGTGGGAAAGTCCCAAATGACAAATGTTGACGCTTGACGTTCTGAGCTT 295		
QY	198 GAGATCATTGAAACATGGGAGCAAATGGTGTCTAACTGGCTCTAACCAT 257		
Db	296 AAATGAAATACAAAATGAGATGACTTGTCAATGAGATGTTGCAATACAAAT 355		
QY	258 GATATTGCTGGTGTGGGAGGACTACACTGTGTTGACGTTGACGACAGCTT 317		
Db	356 GAACAGCTGGGGAGGACTACACTGTGTTGACGTTGACGACAGCTT 415		
QY	318 GCAATTAATGCGACGCGAGTGTGTTGACGTTGACGAGATGAAACA 377		
Db	416 GGCTTGGAGGATTAAGGAGTGTGTTGACGTTGACGAGGAGGTGATTTA 475		
QY	378 GCAACACAGCGTGTGACACCTGAAAGCAGTGTGCAACTGTGTCAGGAA 437		
Db	476 GCTGTGATGCTGTTGATTGTCACTTAAGACACTCTAATCTGGACACCCCTGAA 535		
QY	438 GCTTGTCTCGGGCGCGAGTGTGTTGACGTTGACGTTGACGAGTGTGATG 494		
Db	536 GAAATGCAAGGTTGCGACGTTGCAAGAACGGGAATAAGAATGGCCATATCATC 595		
RESULT	15		
AL515579	AL515579 LTI_NFL011 NBCI Homo sapiens cDNA clone CS00A002YD20 5	1017 bp mRNA	Linear EST 13-FEB-2001
DEFINITION	prime, mRNA sequence.		
ACCESSION	AL515579		

OY	495	T C A G A G G T C A T G G A C C G T G T G G C A C G A T G G T G A T T A C C A T C G A G A A T C T C G A G G T	554
Db	596	T C T G T G C A A T G C A A T G A A M G T G G A C A A G G T G T C A T C A C A G T A A G G T G G A A A C A	655
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OY	615	T A C A T G G T C A C A G A C A T G A M A A M A T G G T G C A G A C C T G A A R A C C A T T A C T T A T C	674
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OY	675	A C G G A T A A A A A G T C A A C T C C A A G A C A T T C C A C T A C T C A C T C A G G A G T C T I A A	734
Db	776	A G T G A A A A G A D A T T C H A G T A T C C A G T C A M G T A C C G C T T C A A T T G C C A T G C T	835
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OY	855	G A 856	
Db	956	G A 957	

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